



Figure 16: Multiple Sequence Alignments of Mil.1, Mil.2 and Rpi-blb2 nucleic acids

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: Mil.1 3768 bp
 Sequence 2: Mil.2 3774 bp
 Sequence 3: Rpi-blb2 3804 bp
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 95
 Sequences (1:3) Aligned. Score: 89
 Sequences (2:3) Aligned. Score: 89
 Guide tree file created: [/ebi/externserv/clustalw-work/interactive/clustalw-20040503-14435620.dnd]
 Start of Multiple Alignment
 There are 2 groups
 Aligning...
 Group 1: Sequences: 2 Score: 68908
 Group 2: Sequences: 3 Score: 65855
 Alignment Score 66872
 CLUSTAL-Alignment file created [/ebi/externserv/clustalw-work/interactive/clustalw-20040503-14435620.aln]

CLUSTAL W (1.82) multiple sequence alignment

Mil.1	ATGGAAAAACGAAAAGATAATGAAGAAAGCAAACTCATTGGTGTCTATTTCTGCTCTT	60
Mil.2	ATGGAAAAACGAAAAGATAATGAAGAAAGCAAACTCATTGGTGTCTATTTCTGCTCTT	60
Rpi-blb2	ATGGAAAAACGAAAAGATAATGAAGAAAGCAAACTCATTGGAGTCAATTTCTGCTCTT	60
*****		*****

Mi1.1	AGCAAGGACATGCCGATGTTCTGGTTTTCCTAGAGA-----ATGAGGAAAATCAA	111
Mi1.2	AGCAAGGACATTGCCAATGTTCTAAATTTTCCTAGAGA-----ATGAGGAAAATCAA	111
Rpi-blb2	CGCAAGGATGCTGCCAATGTTCTGGATTTCCTAGAGAGATTAAAGAATGAAAGATCAA	120

Mi1.1	AAAGCTCTTGACAAAGATCAAGTTGAAAAGATAAAAATTGAAAATGGCATTATTGTACA	171
Mi1.2	AAAGCTCTTGACAAAGATCAAGTTGAAAAGCTAAAAATTGAAAATGGCATTATTGTACA	171
Rpi-blb2	AAGGCTGTTGATGTGGATCTGATTGAAAGCCTGAAATTGAAAGCTGACATTATTGTACA	180
	** ***	
Mi1.1	TATGTTCAGCTTCTTGTTCCGATTTTGAGCAGTTTGAAAGATATAATGACTAGAAAAAGA	231
Mi1.2	TATGTTCAGCTTCTTATTCCGATTTTGAGCAGTTTGAAAGATATAATGACTAGAAAAAGA	231
Rpi-blb2	TATGTCCAGCTTCTTATTCCGATTTTGGAGAAAGTTTGAAGATATAATGACTAGAAAAAGA	240

Mi1.1	CAAGAGGTTGAGAACTCTGCTTCAACCACCTTTTGGATGATGATG-----	274
Mi1.2	CAAGAGGTTGAGAACTCTGCTTCAATCACTTTTGGATGATGATG-----	274
Rpi-blb2	CAAGAGGTTGAGAACTCTGCTTCAACCAATTTTGGATGATGATGGCAAAGACGTCGGGTGT	300

Mi1.1	-----TCTTTACTAGCCTCACCGTAATAATGGATGACTGTATCAGCTTGTATCATCGT	327
Mi1.2	-----TCCTTACTAGCCTCACCGTAATAATGGATGACTGTATCAGCTTGTATCATCGT	327
Rpi-blb2	AAATATGTCCTTACTAGCCTCGCCGGTAATAATGGATGACTGTATAAGCTTGTATCATCGT	360
	** *****	
Mi1.1	TCTTATAAATCAGATGCCATCATGATGGATGAGCAATTGGACTTCCTCCTCTTGAATCTC	387
Mi1.2	TCTTATAAATCAGATGCCATCATGATGGATGAGCAATTGGACTTCCTCCTCTTGAATCTG	387
Rpi-blb2	TCT---AAATCAGATGCCACCATGATGGATGAGCAATTGGGCTTCCTCCTCTTGAATCTC	417
	*** *****	

Mi1.1	TATCATCTATCCAAGCATCAGGCTGAAAAGATATTTCTCTGGAGTGACTCAATATGAAGTT	447
Mi1.2	TATCATCTATCCAAGCATCAGGCTGAAAAGATATTTCTCTGGAGTGACTCAATATGAAGTT	447
Rpi-blb2	TCTCATCTATCCAAGCATCGTGTGAAAAGATGTTTCTCTGGAGTGACTCAATATGAAGTT	477
	* ****	***
Mi1.1	CTTCAGAATATATGTGGCAACATAAGAGATTTCCATGGGTTGATAGTGAATGGTTGCATT	507
Mi1.2	CTTCAGAATGTATGTGGCAACATAAGAGATTTCCATGGGTTGATAGTGAATGGTTGCATT	507
Rpi-blb2	CTTCAGAATGTATGTGGCAACATAAGAGATTTCCATGGATTTGATAGTGAATGTTGCATT	537
	*****	*****
Mi1.1	AAGCATGAGATGTTGAGAATGTCTTRCCTCTGTCTTCACTCATGGCTGACAGAGTAGGA	567
Mi1.2	AAGCATGAGATGTTGAGAATGTCTTACCTCTGTCTTCACTCATGGCTGAAAAGAGTAGGA	567
Rpi-blb2	AAGCATGAGATGTTGAGAATGTCTTATCTCTGTCTTCACTGATGGCTGAGAGAGTAGGA	597
	*****	*****
Mi1.1	CAC TTCCTTTGGGATGATCAGACTGATGAAGACTCTCGACTCTCCGAGCTAGATGAGGAT	627
Mi1.2	CAC TTCCTTTGGGAGGATCAGACTGATGAAGACTCTCGGCTCTCCGAGCTAGATGAGGAT	627
Rpi-blb2	CGCTTCCTTTGGGAGGATCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGATGAGGAT	657
	* ****	*****
Mi1.1	GAACAAAATGATAGAGACTCTCGACTTTTCAAGCTAGCACATCTACTCTTGAAGATCGTT	687
Mi1.2	GAACACAATGATAGAGACTCTCGACTCTTCCAGCTAACACATCTACTCTTGAAGATTGTT	687
Rpi-blb2	GATCAGAATGATAAAGACCCTCAACTCTTCAAGCTAGCACATCTACTCTTGAAGATTGTT	717
	** **	***
Mi1.1	CCGGTTGAAC TGGAGGTTATACACATATGTTATACAAAATTGAAAGCTTCAACTTCAGCT	747
Mi1.2	CCAACTGAACTGGAGGTTATGCACATATGTTATACAAAATTGAAAGCTTCAACTTCAGCA	747
Rpi-blb2	CCAACTGAAATTGGAGGTTATGCACATATGTTATAAAACTTTGAAAGCTTCAACTTCAACA	777
	** ****	*****
Mi1.1	GAAGTTGGACTCTTTCATTAAGCAGCTTCTAGAAAACCTCTCCAGATATTTCTGAGGGAATAT	807

Mi1.2	GAAGTTGGACGCTTCATTAAGAAGCTCCTGGAAACCTCACCGGATATTCTCAGAGAAATAT	807
Rpi-blb2	GAAATTGGACGCTTCATTAAGAAGCTCCTGGAAACCTCTCCGGACATTCTCAGAGAAATAT	837
	*** *****	*** ** ***** ** ***** ** *****
Mi1.1	CTAATTCTCTGCAAGAGCACATGGTAACGTGTTATTACCCCTAGCACCTTCAGGGGCTCGA	867
Mi1.2	ATCATTTCAACTACAAGAGCATATGTTAACTGTTATTCCCTTAGCACCTTAGGGGCTCGA	867
Rpi-blb2	CTGATTTCATCTACAAGAGCATATGATAACTGTTATTACCCCTAACACTTCAGGGGCTCGA	897
	* **** ** *****	*** ***** ***** ***** ***** *****
Mi1.1	AACATTTCATGTCATGATGGAAATTCCTATTACTTATTCTTTCTGTATATGCC--CAAGGAC	924
Mi1.2	AACATTTCATGTCATGATGGAAATTCCTATTACTTATTCTTTCTGTATATGCC--CAAGGAC	924
Rpi-blb2	AACATTTCATGTCATGATGGAAATTCCTATTGATTTATTCTTTCTGTATATGCCGCCCAAGGAC	957
	*****	***** ***** ***** ***** *****
Mi1.1	TTTATTTCATCATGACAAACTTTTGTGATCTCTTGGATCGTGTGGAGTACTTACCAGGGAG	984
Mi1.2	TTTATTTCATCATGACAAACTTTTGTGATCTCTTGGCTCATGTTGGAACACTTACCAGGGAG	984
Rpi-blb2	TTTATTTCATCATGACAAACTTTTGTGATCTCTTGGCTCGTGTGTAGCACTTACCAGGGAG	1017
	*****	***** ***** ***** ***** *****
Mi1.1	GTATCAACTCTTGTACGTGACTTGGAAAGAGGAACCAAGGAATAAAGAGGGTAATAACCAA	1044
Mi1.2	GTATCGACTCTTGTACGTGACTTGGAAAGAGAAATTAAGGAATAAAGAGGGTAATAACCAA	1044
Rpi-blb2	GTATCAACTCTTGTACGCGACTTGGAAAGAGAAATTAAGGATTAAGAGAGTACTGACGAA	1077
	*****	***** ***** ***** ***** *****
Mi1.1	ACAAATTGTGCAACCCCTAGACTTGTGTGGAAAAATATTGAACTCCTCAAGAAAGATCTCAA	1104
Mi1.2	ACAAATTGTGCAACCCCTAGACTTGTGTGGAAAAATATTGAACTCCTCAAGAAAGATCTCAA	1104
Rpi-blb2	ACAAATTGTGCAACCCCTAAAGTTTCTGTGGAAAAATATTGAACTCCTTAAGGAAGATCTCAA	1137
	*****	***** ***** ***** ***** *****
Mi1.1	CATGTTTATCTGAAAGCCCTGGATTCACTCAATGTTGCTTCCCATGAGTGATGGACCA	1164
Mi1.2	CATGTTTATCTGAAAGCCCCAAATTCATCTCAATGTTGCTTCCCATGAGTGATGGACCA	1164

Rpi-blb2	CATGTTTATCTGAAAAGTCCCGGATTTCATCTCAATATTGCTTCCCATGAGTGATGGACCT 1197
	***** ** *****
Mil1.1	CTCTTCATGCATCTTCTACACATACACTTAAATGATTGTGTAGATTCTAATGCTTATTCA 1224
Mil1.2	CTCTTCATGCATCTTCTACACATGCACCTAAATGATTGTGTAGATTCTAATGCTTATTCA 1224
Rpi-blb2	CTCTTCATGCATCTGCTACAGAGACACTTAGATGATTGTGTGGATTCCAATGCTTATTCA 1257
	***** ** *****
Mil1.1	ATTGCTTTGATAAAGGAAGAAATCGAGCTGGTGAAGCAAGACCTGAAATTCATAAGATCA 1284
Mil1.2	ATTCTTTTGATAAAGGAAGAAATCGAGTTGGTGAGTCAAGAACTGGAATTCATAAGATCA 1284
Rpi-blb2	ATTGCTTTGATAAAGGAACAAATTGGGCTGGTGAAAGAAAGACTTGGAAATTCATAAGATCT 1317
	*** ***** ** *****
Mil1.1	TTCTTTTGTGGATGCTG--AGCAAGGATTGTATAAAGATCTCTGGGCACGTGTTCTAGAT 1341
Mil1.2	TTCTTTGGGATGCTGCTGAGCAAGGATTGTATAAAGATATCTGGGCACGTGTTCTAGAT 1344
Rpi-blb2	TTTTTCGCGAATATTG--AGCAAGGATTGTATAAAGATCTCTGGGAACGTGTTCTAGAT 1374
	** ** * ** *****
Mil1.1	GTGGCTTATGAGGCAAAAGATGTCATAGATTCAATTATTGTTTCGAGATAAATGGTCTCTTA 1401
Mil1.2	GTGGCTTATGAGGCAAAAGATGTCATAGATTCAATTATTGTTTCGAGATAAATGGTCTCTTA 1404
Rpi-blb2	GTGGCATATGAGGCAAAAGATGTCATAGATTCAATTATTGTTTCGAGATAAATGGTCTCTTA 1434
	***** *****
Mil1.1	CATCTTATTTTCTCACTTCCCATTACCATAAAGAAGATCAAACTTATCAAAAGAAGAGATC 1461
Mil1.2	CATCTTATTTTCTCACTTCCCATTACCATAAAGAAGATCAAACTTATCAAAAGAAGAGATC 1464
Rpi-blb2	CATCTTATTTTCTCACTTCCCATTACCAGAAAGAAGATGATGCTTATCAAAAGAAGAGGTC 1494
	***** *****
Mil1.1	TCTGCTTTTAGATGAGAACATTCCCAAGGACAGAGGTCTAATCGTTGTGAACCTCTCCCAAG 1521
Mil1.2	TCTGCTTTTAGATGAGAACATTCCCAAGGACAGAGGTCTAATCGTTGTGAACCTCTCCCAAG 1524
Rpi-blb2	TCTGATTTACATGAGAACATTTCCAAGAACAGAGGTCTCATCGTTGTGAACCTCTCCCAAG 1554

Amendment dated October 24, 2007

Reply to Office Action of April 24, 2007

Annotated Sheets Showing Changes

Mi1.1
AAACCAAGTTGAGAGAAAGTCATTGACAACTGATAAAATAACTGTAGGTTTTCAGGAGGAA 1581

Mil.2 AAACCACTTGAGAGAAAGTCATTGCAACTGATAAAATAATTGTAGGTTTGTAGGAGGAG 1584

Rp1-blb2
AAACCAGTTGAGAGCAAGTCATTGACAACTGATAAAATAATTGTAGGTTTTGGTGAGGAG 1614

Mil.1
ACAAACTTGATACCTTAGAAAGCTCACCAAGTGGATCGGCAGATCTAGATGTCATTTCGATC 1641

mi1.2
ACAAACTTGATACCTTAGAAAGCTCACCGAGTGGACCCGAGATTTAGATGTCATTTTCGATC 1644

Rpi-blb2
ACAAACTTGATACCTTAGAAAGCTCACCAGTGGACCGCAGATCTAGATGTCATTTTCGATC 1674

Mi1.1
ACTGGTATGCCGGGTTCAGGTAAACTACTTTGGCATACAAAGTATACAATGATAAGTCA 1701

Mi1.2
ACCGGTATGCCGGGTTCAGGTAAACTACTTTGGCATACAAAGTATACAATGATAAGTCA 1704

Rpi-blb2
ATTGGTATGCCGGGTTTAGGTAAACTACTTTGGCGTACAAAGTATACAATGATAAATCA 1734

[illegible]

Mil.1
GTTTCTAGCCGTTTCGACCTTCGTGCATGGTGCACGGTCGACCAAGGATGTGATGAGAAG 1761

Mi1.2 GTTCCTAGACATTTTGACCTTCGTGCATGTCACGGTCGATCAAGGATATGACGACAAG 1764

Rpi-blb2
GTTTCTAGCCATTTCGACCTTCGTGCATGGTGCACGGTCGACCAAGTATATGACGAGAAG 1794

1821

mi1.2 AAGTTGTTGGATACAAATTTTCAGTCAAGTTAGTGGCTCAGATTCAAATTTTGAGTGAGAAT 1824

Rpi-blb2 AAGTTGTTGGATAAAATTTTCAATCAAGTTAGTGACTCAAATTCAAAAATTGAGTGAGAAAT 1854

[illegible]

Mil.1
 ATTGATGTTGCTGATAAATTACGGAAACAACACTGTTTGGAAGAGGTATCTTATTGTCTTA 1881

ATGATGTTGCTGATAAATTGCGGAAACAACACTGTTTGGAAGAGGTATCTTATTGTCTTA 1884

Rp1-blb2
ATTGATGTTGCTGATAAATAACGGAACAATTGTTTGGAAAGAGGTATCTTATTGTCTTA 1914

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Mi1.1	GATGACGTGTGGGATACTACTACATGGGATGAGTTAAACAAGACCTTTTCCTGAATCTAAG	1941
Mi1.2	GATGATGTGTGGGATACTACTACATTTGGATGAGTTGACAAGACCTTTTCCTGAAGCTAAG	1944
Rpi-blb2	GATGACGTGTGGGATACTAAATACATGGGATGAGCTAAACAAGACCTTTTCCTGATGGTATG	1974
	*****	*****
	*****	*****
	*****	*****
Mi1.1	AAAGGAAGTAGGATTATTTTGACAACCTCGGGAAGGAAGTGCTTTGCATGGAAAGCTG	2001
Mi1.2	AAAGGAAGTAGGATTATTTTGACAACCTCGAGAAAAGGAAGTGCTTTGCATGGAAAGCTG	2004
Rpi-blb2	AAAGGAAGTAGAATTATTTTGACAACCTCGAGAAAAGGAAGTTGCTTTGCATGGAAAGCTC	2034
	*****	*****
	*****	*****
	*****	*****
Mi1.1	AACACTGATCCTCTTGACCTTCGATTGCTAAGACCAGATGAAAGTTGGGAACCTATTAGAG	2061
Mi1.2	AACACTGATCCTCTTGACCTTCGATTGCTAAGACCAGATGAAAGTTGGGAACCTTTTAGAT	2064
Rpi-blb2	TACACTGATCCTCTTAACCTTCGATTGCTAAGATCAGAAAGAAAGTTGGGAGTTATTAGAG	2094
	*****	*****
	*****	*****
	*****	*****
Mi1.1	AAAAGGGCATTTGGGAATGAGAGTTGCCCTGATGAACCTATTAGATGTCGGTAAAGAAATA	2121
Mi1.2	AAAAGGACATTTGGTAATGAGAGTTGCCCTGATGAACCTATTAGATGTCGGTAAAGAAATA	2124
Rpi-blb2	AAAAGGGCATTTGGAAACGAGAGTTGCCCTGATGAACCTATTGGATGTTGGTAAAGAAATA	2154
	*****	*****
	*****	*****
	*****	*****
Mi1.1	GCCGAAAATTGTAAAGGGCTTCCTTTTGGTGGCTGATCTGATTGCTGGAGTCATTGCTGGG	2181
Mi1.2	GCCGAAAATTGTAAAGGGCTTCCTTTTGGTGGCTGATCTGATTGCTGGAGTCATTGCTGGG	2184
Rpi-blb2	GCCGAAAATTGTAAAGGGCTTCCTTTTGGTGGTGGATCTGATTGCTGGAATCATTGCTGGG	2214
	*****	*****
	*****	*****
	*****	*****
Mi1.1	AGGGAAAAGAAAAGGAGTGTGTGGCTTGAAGTTCAAAGTAGTTTGAGTCTTTTATTTTG	2241
Mi1.2	AGGGAAAAGAAAAGGAGTGTGTGGCTTGAAGTTCAAAGTAGTTTGAGTCTTTTATTTTG	2244
Rpi-blb2	AGGGAAAAGAAAAGGAGTGTGTGGCTTGAAGTTGTAATAATTGCAATTCCTTTATTTTG	2274
	*****	*****
	*****	*****
	*****	*****

Mi1.1	AACAGTGAAGTGGAAGTGATGAAAGTTATAGAATTAAAGTTATGACCAATTACCACATCAC	2301
Mi1.2	AACAGTGAAGTGGAAGTGATGAAAGTTATAGAATTAAAGTTATGACCAATTACCACATCAC	2304
Rpi-blb2	AAGAAATGAAGTGGAAGTGATGAAAGTTATAGAATAAAGTTATGACCACTTACCTGATCAC	2334
	** * *****	*****
Mi1.1	CTCAAGCCATGCTTGCTGTATTTTGCAAGTTTCCGAAGGACACTTCATTGACAATCTAT	2361
Mi1.2	CTCAAGCCATGCTTGCTTCACTTTTGCAAGTTGGCCGAAGGACACTCCTTTGACAATCTAT	2364
Rpi-blb2	CTGAAGCCATGCTTGCTGTACTTTTGCAAGTGCGCCGAAGGACTGGGTAACGACAATCCAT	2394
	** *****	*****
Mi1.1	GAGTTGAATGTTTATTTCGGTGCTGAAGGATTTGTGGGAAAGACGGAGATGAACAGTATG	2421
Mi1.2	TTGTTTACTGTTTATTTCGGTGCTGAAGGATTTGTGGAAAGACGGAGATGAAGGGTATA	2424
Rpi-blb2	GAGTTGAAACTTATTTCGGGTTTGAAGGATTTGTGGAAAGACAGATATGAAGAGTCTG	2454
	*** * ** **	*****
Mi1.1	GAAGAAGTGGTGAAGATTATATGGATGATTTAATTACAGTAGCTTGGTAAATTTGTTTC	2481
Mi1.2	GAAGAAGTGGTGAAGATTATATGGATGATTTAATTCCAGTAGCTTGGTAAATTTGTTTC	2484
Rpi-blb2	GAAGAAGTGGTGAAGAAATTTATTTGGATGATTTAATTCCAGTAGCTTGGTAAATTTGTTTC	2514
	*****	*****
Mi1.1	AATGAGATAGGTTATGCACCTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTGTTG	2541
Mi1.2	AATGAGATAGGTGATATACTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTGTTG	2544
Rpi-blb2	AATGAGATAGGTGATTAACCTACTTGCCAACTTCATGATCTTGTGCATGACTTTTGTGTTG	2574
	*****	*****
Mi1.1	ATAAAAGCAAGAAAGGAAAAATTTGTTTGATCAGATAAAGATCAAGTGCTCCATCAGATTG	2601
Mi1.2	ATAAAAGCAAGAAAGGAAAAATTTGTTTGATCGGATAAAGATCAAGTGCTCCATCAGATTG	2604
Rpi-blb2	ATAAAAGCAAGAAAGGAAAAAGTTGTGTGATCGGATAAAGTTCAAGTGCTCCATCAGATTG	2634
	*****	*****
Mi1.1	TTGCCTCGTCAAATTACCATTGATTGTGATGAGGAGGAG - - - CACTTTGGGCTTAATTT	2658

Mi1.2	TTGCCCTCGTCAAATTACCATTTGATTATGATGAGGAGGAGCACCTTTGGGCTTAATTTT	2664
Rpi-blb2	TTGCCACGTCAAATTAGCATTTGATTATGATGATGATGAAGAGCACCTTTGGGCTTAATTTT	2694
	*****	*****
Mi1.1	GTCATGTTTCGATTCAAATAAGAAAAGGCATTCTGGTAAACACCTCTATTCTTTGAGGATA	2718
Mi1.2	GTCATGTTTCGATTCAAATAAGAAAAGGCATTCTGGTAAACACCTCTATTCTTTGAGGATA	2724
Rpi-blb2	GTCCGTGTTTCGGTTCAAATAAGAAAAGGCATTCCGGTAAACACCTCTATTCTTTGACCATA	2754
	*****	*****
Mi1.1	ATTGGAGACCAGCTGGATGACAGTGTCTCTGATGCATTTCACTAAGACACTTGAGGCTT	2778
Mi1.2	AATGGAGACCAGCTGGATGACAGTGTCTCTGATGCATTTCACTAAGACACTTGAGGCTT	2784
Rpi-blb2	AATGGAGATGAGCTGGACGACCATCTTCTGATACATTTTCATCTAAGACACTTGAGGCTT	2814
	* *****	*****
Mi1.1	CTTAGAGTGTGGACCTGCATACCGTCTTTTATCATGGTGAAAGATTCTTTTGCTGAATGAA	2838
Mi1.2	ATTAGAGTGTGGACCTGGAAACCTCTTTAATCATGGTGAATGATTCTTTGCTGAATGAA	2844
Rpi-blb2	CTTAGAAACCTTGCACCTGGAATCCTCTTTTATCATGGTTAAAGATTCTTTGCTGAATGAA	2874
	*****	*****
Mi1.1	ATATGCATGTTGAATCATTTGAGGTACTTATCCATTGACACACAAGTTAAATATCTGCCT	2898
Mi1.2	ATATGCATGTTGAATCATTTGAGGTACTTAAAGAAATTCGGACACACAAGTTAAATATCTGCCT	2904
Rpi-blb2	ATATGCATGTTGAATCATTTGAGGTACTTAAAGCATTTGGGACAGAAGTTAAATCTCTGCCT	2934
	*****	*****
Mi1.1	TTGTCCTTTCTCAAACCTCTGGAATCTAGAAAGCCTGTTTGTGTCTACCAACAGATCAATC	2958
Mi1.2	TTCTCTTTTCTCAAACCTCTGGAATCTAGAAAGTCTGTTTGTGTCTAACAAGGATCAATC	2964
Rpi-blb2	TTGTCCTTTCTCAAACCTCTGGAATCTAGAAATCTTGTTTGTGGATAACAAGAATCAACC	2994
	** *****	*****
Mi1.1	TTGGTACTATTACCGAGAAATTTTGGATCTTGTAAAGTTGCGAGTGCTGTCCGTGGATGCT	3018
Mi1.2	TTGGTACTATTACCGAGAAATTTTGGATCTTGTAAAGTTGCGAGTGCTGTCCGTGGTGCT	3024

Rpi-blb2	TTGATACTATTACCGAGAAATTTGGGAICTTTGTAAAGTTTGCAAGTGTCTGTTCAAGACTGCT 3054 *** *****
Mil.1	TGTTCTTTCTTTTGATAATGGATGCAGATGAATCAATATTGATAGCAGAGGACACAAAAGTTA 3078
Mil.2	TGTTCTTTCTTTTGATAATGGATGCAGATGAATCAATATTGATAGCAGAGGACACAAAAGTTA 3084
Rpi-blb2	TGTTCTTTCTTTTGATAATGGATGCAGATGAATCAATATTGATAGCAGAGGACACAAAAGTTA 3114 *****
Mil.1	GAGAACTTGAGAATATTAACGGAACTGTGTGATTTCCCTATTTCGAAAGATACAAAGAAATATT 3138
Mil.2	GAGAACTTGAGAATATTAAGGGAACTGTGTGATTTCCCTATTTCGAAAGATACAAATGAATATT 3144
Rpi-blb2	GAGAACTTGACAGCATTAGGGGAACTCGTGTCTTTCCCTATTGGAAGATACAGAGGATATT 3174 *****
Mil.1	TTCAAAAGGTTTCCCAATCTTCAGTTGCTTTTCATTTGAACTCAAGGAGTCATGGGATTAT 3198
Mil.2	TTCAAAAGGTTTCCCAATCTTCAGGTGCTTCAGTTTGAAGTCAAGGAGTCATGGGATTAT 3204
Rpi-blb2	TTCAAAAGGCTTCCCAATCTTCAAGTGCTTCATTTCAAACTCAAGGAGTCATGGGATTAT 3234 *****
Mil.1	TCAACAGAGCAACATTGGTTCTCGGAAATTGGATTTCCTAACTGAAC TAGAAACACTCTCT 3258
Mil.2	TCAACAGAGCAACATTGGTTCCCGAAATTGGATTGCCTAACTGAAC TAGAAACACTCTGT 3264
Rpi-blb2	TCAACAGAGCAATATTGGTTCCCGAAATTGGATTTCCTAACTGAAC TAGAAACACTCACT 3294 *****
Mil.1	GTAGGTTTAAAGTTCAAAACACAAACGATAGTGGTCCCTCTGTAGCGACAAATCGGCCG 3318
Mil.2	GTAGGTTTAAAGTTCAAAACACAAACCACTGTGGTCCCTCTGTGTGACAAATCGGCCG 3324
Rpi-blb2	GTAGATTTTGAAAGATCAAAACACAAATGACAGTGGTCCCTCTGCAGCCATAAAATCGGCCA 3354 *****
Mil.1	TGGGATTTTCACTTCCCTTCAAATTTGAAAATACTGTGTTGCCGTGAATTTCCGCTGACA 3378
Mil.2	TGGGATTTTCACTTCCCTTCAAATTTGAAAGAACTGTGTGTGATGACTTTTCCCTCTGACA 3384
Rpi-blb2	TGGGATTTTCACTTTCCTTCGAGTTTGAAAAGATTGCAATTGCATGAATTTTCCCTCTGACA 3414

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Mi1.1	TCCGATTCACTATCAACAATAGCGAGACTGCCCAACCTTGAAGAGTTGTCCCTTTATCAT	3438										
Mi1.2	TCCGATTCACTATCAACAATAGCGAGACTGCCCAACCTTGAAGAAATTTGTCCCTTTATGAT	3444										
Rpi-blb2	TCCGATTCACTATCAACAATAGCGAGACTGCTGAACCTTGAAGAGTTGTACCTTTATCGT	3474										
	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*	
Mi1.1	ACAATCATCCATGGAGAAGAAATGGAACATGGGGAGGAAGACACCTTTGAGAATCTCAAA	3498										
Mi1.2	ACAATCATCCAGGAGAAGAAATGGAACATGGGGAGGAAGACACCTTTGAGAATCTCAAA	3504										
Rpi-blb2	ACAATCATCCATGGGGAAGAAATGGAACATGGGAGAAAGACACCTTTGAGAATCTCAAA	3534										
	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	
Mi1.1	TTTTTTGAACTTCAATCAAGTTAGTATTTCCAAGTGGGAGGTTGGAGAGGAATCCTTCCCC	3558										
Mi1.2	TTTTTTGAACTTGGCTACTGACTCTTTCCAAGTGGGAGGTTGGAGAGGAATCCTTCCCC	3564										
Rpi-blb2	TGTTTGATGTTGAGTCAAGTGATTCTTTCCAAGTGGGAGGTTGGAGAGGAATCTTTTCCC	3594										
	*	*****	**	**	*	*	*	*	*	*****	**	***
Mi1.1	AATCTTGAGAAATTAAACTGCGGGGATGTCATAAGCTAGAGGAGATTCCACCTAGTTT	3618										
Mi1.2	AATCTTGAGAAATTAAACTGCAGGAATGTGTAAGCTTGAGGAGATTCCACCTAGTTT	3624										
Rpi-blb2	ACGCTTGAGAAATTAGAACTGTCTGGACTGTCATAAATCTTGAGGAGATTCCGCTAGTTT	3654										
	*	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
Mi1.1	GGAGATATTTATTCATTGAAATCTATCAAAATTGTAAAGAGTCCTCAACTTGAAGATTCT	3678										
Mi1.2	GGAGATATTTATTCATTGAAATTTATCAAAATTGTAAAGAGTCCTCAACTTGAAGATTCT	3684										
Rpi-blb2	GGGGATATTTATTCCTTGAAATTTATCGAACTTGTAAGGAGCCCTCAACTTGAAAAATCC	3714										
	**	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
Mi1.1	GCTCTCAAAATTAAGGAATACGCTGAAGATATGAGGGGAGGGACGAGCTTCAGATCCTT	3738										
Mi1.2	GCTCTCAAGATTAAGAAATACGCTGAAGATATGAGAGGAGGGAACGATCTTCAGATCCTT	3744										
Rpi-blb2	GCTCTCAAGATTAAGGAATATGCTGAAGATATGAGGGGAGGGACGAGCTTCAGATCCTT	3774										
	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****

Mi1.1	GGCCAAAAGAATATCCCCCTTATTTAAGTAG	3768
Mi1.2	GGCCAGAAGAATATCCCCCTTATTTAAGTAG	3774
Rpi-blb2	GGCCAGAAGGATATCCCGTTATTTAAGTAG	3804
	*****	*****